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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: Wed Jun 13 09:40:20 EDT 2007

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Application No: 10586045 Version No: 1.1

Input Set:

Output Set:

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Finished: 2007-06-13 09:40:03.821
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Total Errors: 0
No. of SeqIDs Defined: 45
Actual SeqID Count: 45

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Input Set:

Output Set:

Started: 2007-06-13 09:40:02.726
Finished: 2007-06-13 09:40:03.821
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 95 ms
Total Warnings: 31
Total Errors: 0
No. of SeqIDs Defined: 45
Actual SeqID Count: 45

| Error code | Error Description |
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SEQUENCE LISTING

<110> Korea Research Institute of Bioscience and Biotechnology
Sohn, Jung-Hoon
Choi, Eui-Sung
Bae, Jung-Hoon
Lee, Eung-Suck
Shin, Mi-Kyung

<120> Rapid screening method of translational fusion partners for
producing recombinant proteins and translational fusion partners
screened therefrom

<130> 2472.0010000

<140> US 10/586,045
<141> 2006-07-14

<150> PCT/KR2004/003517
<151> 2004-12-30

<150> KR 10-2004-0003610
<151> 2004-01-17

<150> KR 10-2004-0003957
<151> 2004-01-19

<160> 45

<170> PatentIn version 3.3

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<222> (1)..(105)
<223> TFP1

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20 25 30

Ala Asp Leu Ser Ser Ile Thr Ser Val Ser Ser Ala Ser Ala Ser Ala
35 40 45

Thr Ala Ser Asp Ser Leu Ser Ser Ser Asp Gly Thr Val Tyr Leu Pro

50

55

60

Ser Thr Thr Ile Ser Gly Asp Leu Thr Val Thr Gly Lys Val Val Ile Ala
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Gly Glu Lys Tyr Val Phe Ser Ser Asp
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aatcgaaaaa acaaattcca agctgctgtc gctttggccc tactctctcg cggcgctctc 180
ggtgactctt acaccaatag cacctccccc gcagacttga gttctatcac ttccgtctcg 240
tcagcttagtg caagtgccac cgcttccgac tcactttctt ccagtgacgg taccgtttat 300
ttgccatcca caacaattag cggtgatctc acagttactg gttaaagtaat tgcaaccgag 360
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<222> (1)..(117)
<223> TFP2

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1 5 10 15

Val Ser Ala Leu Gln Val Asn Asn Ser Cys Val Ala Phe Pro Pro Ser
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Asn Leu Arg Gly Lys Asn Gly Asp Gly Thr Asn Glu Gln Tyr Ala Thr
35 40 45

Ala Leu Leu Ser Ile Pro Trp Asn Gly Pro Pro Glu Ser Leu Arg Asp
50 55 60

Ile Asn Leu Ile Glu Leu Glu Pro Gln Val Ala Leu Tyr Leu Leu Glu
65 70 75 80

Asn Tyr Ile Asn His Tyr Tyr Asn Thr Thr Arg Asp Asn Lys Cys Pro
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100 105 110

Arg Ser Leu Asn Asp
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gtgagcgcac tccaggtcaa caattcatgt gtcgcatttc cgccatcaaa tctcagaggc 180
aaaaatggag acggtaactaa tgaacagtat gcaactgcac tactttctat tccctggaaat 240
ggacctcctt gtcatttgag ggatattaat cttattgaac tcgaaccgca agttgcactc 300
tatttgctcg aaaatttat taaccattac tacaacacca caagagacaa taagtgcctt 360
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<222> (1)..(104)
<223> TFP3

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Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr
35 40 45

Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg
50 55 60

Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala
65 70 75 80

Ala Thr Ala Gln Ala Thr Asp Ser Gln Ala Gln Ala Thr Thr Thr Ala
85 90 95

Thr Pro Thr Ser Ser Glu Lys Ile
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<400> 6

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| gcccaaaaaga | aacgggtcag | cgtgtactgc | gccaaaaaaaaa | tgcgcgcga | tttaagctaa | 120 |
| acgtccacaa | acaaaaacaa | aaataagaaa | taggttgaca | gtgggtgaaa | aattctcgaa | 180 |
| ggtttcatct | ccaaacagtc | agtatataag | tattcggaa | agagagccaa | tctatcttgt | 240 |
| ggtggtctta | tcttaacctt | ctcttttgg | cagtagtaat | tgttaatcaa | gacacataaa | 300 |
| actatccac | tcgctaaact | tacatctaaa | atgcaattca | aaaacgtcgc | cctagctgcc | 360 |
| tccgttgctg | ctctatccgc | cactgcttct | gctgaagggtt | acactccagg | tgaaccatgg | 420 |
| tccaccttaa | cccccaaccgg | ctccatctct | tgtggtgctg | ccgaatacac | taccaccttt | 480 |
| ggtattgctg | ttcaagctat | taccttttca | aaagctaaga | gagacgttat | ctctcaaatt | 540 |
| ggtgacggtc | aagtccaaagc | cacttctgct | gctactgctc | aagccaccga | tagtcaagcc | 600 |
| caagctacta | ctaccgctac | cccaaccagg | tccgaaaaga | tc | | 642 |

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 <213> Hansenula polymorpha

<220>
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 <222> (1)..(50)
 <223> TFP4

<400> 7

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| Met | Arg | Phe | Ala | Glu | Phe | Leu | Val | Val | Phe | Ala | Thr | Leu | Gly | Gly | Gly |
| 1 | | | | | | | | | | | | | | | 15 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Pro | Val | Glu | Ser | Leu | Ala | Gly | Thr | Gln | Arg | Tyr | Leu | Val |
| | | | | | | | | | | | | | | | |
| | | | 20 | | | 25 | | | | | 30 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Met | Lys | Glu | Arg | Phe | Thr | Thr | Glu | Lys | Leu | Cys | Ala | Leu | Asp | Asp |
| | | | | | | | | | | | | | | | |
| | | | 35 | | | 40 | | | | | 45 | | | | |

Lys Ile
 50

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 <211> 179
 <212> DNA
 <213> Hansenula polymorpha

<220>
<221> gene
<222> (1)..(179)
<223> TFP4

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tggtgcaaat gaaggagcgg ttcaccacag agaagctgtg tgcttggac gacaagatc 179

<210> 9
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<212> PRT
<213> *Saccharomyces cerevisiae*

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<222> (1)..(71)
<223> TFP1-3

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20 25 30

Ala Asp Leu Ser Ser Ile Thr Ser Val Ser Ser Ala Ser Ala Ser Ala
35 40 45

Thr Ala Ser Asp Ser Leu Ser Ser Asp Gly Thr Val Tyr Leu Pro
50 55 60

Ser Thr Thr Ile Ser Gly Asp
65 70

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acttccgtct cgtcagctag tgcaagtgcc accgcttcg actcacttcc ttccagtgac 180

ggtaccgttt atttgcacatc cacaacaatt agcggtgatc tcacagttac tggtaaagta 240

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aaataacgtct tctcatctga tcctctaga 329

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<210> 12
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<210> 13
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<210> 14
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<223> JH106 (Sfi-IL2-forward primer)

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gcggccatta cggccgtgca cctacttcaa gttctac 37

<210> 16
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<223> JH107 (Sfi-IL2-reverse primer)

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gcggccatta cggccgtgca cctacttcaa gttctac 37

<210> 17
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<213> Artificial Sequence

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<223> JH120 (BamHI-IL2-1-forward primer)

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cgggatccgc acctacttca agttct 26

<210> 18
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<223> JH121 (BamHI-IL2-2-forward primer)

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<210> 19
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<223> JH122 (BamHI-IL2-3-forward primer)

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<211> 22

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<223> JH123 (INV-1-reverse primer)

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<210> 21

<211> 22

<212> DNA

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<223> JH124 (INV-forward primer)

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<210> 22

<211> 29

<212> DNA

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<212> DNA

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<223> JH132 (SacI-GAL-forward primer)

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27

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47

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46

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<210> 30
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47

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27

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<223> JH141 (XbaI-TFP1-b-reverse primer)

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27

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42

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<223> JH144 (GCSF-forward primer)

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<223> HY18 (TFP3-LDKR-forward primer)

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Ala Thr Ala Ser Ala Glu Gly Tyr Thr Pro Gly Glu Pro Trp Ser Thr
20 25 30

Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr
35 40 45

Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg
50 55 60

Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala
65 70 75 80

Ala Thr Ala Gln Ala Thr Asp Ser Gln Ala Gln Ala Thr Thr Ala
85 90 95

Thr Pro Thr Ser Ser Glu Lys Ile Ser Ser Ser Ala Ser Lys Thr Ser
100 105 110

Thr Asn Ala Thr Ser Ser Cys Ala Thr Pro Ser Leu Lys Asp Ser
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Ser Cys Lys Asn Ser Gly
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tgtggtgctg ccgaatacac taccaccttt ggtattgctg ttcaagctat tacctcttca 180

aaagctaaga gagacgttat ctctcaaatt ggtgacggtc aagtccaagc cacttctgct 240

gctactgctc aagccaccga tagtcaagcc caagctacta ctaccgctac cccaaaccagc 300

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Met Gln Phe Lys Asn Val Ala Leu Ala Ala Ser Val Ala Ala Leu Ser
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20 25 30

Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr
35 40 45

Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg
50 55 60

Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala
65 70 75 80

Ala Thr Ala Gln Ala Thr Asp Ser Gln Ala Gln Ala Thr Thr Thr Ala
85 90 95

Thr Pro Thr Ser Ser Glu Lys Ile Ser Ser Ser Ala Ser Lys Thr Ser
100 105 110

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Ser Cys Lys Asn Ser Gly Thr Leu Glu Leu Thr Leu Lys Asp Gly
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tgtggtgctg ccgaatacac ta